

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: April 26, 2005, 20:05:04 ; Search time 2.79577 Seconds
(without alignments)
8779.016 Million cell updates/sec

Title: US-10-750-976-38

Perfect score: 15

Sequence: 1 ctgaacctagggcgca 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	15	3	US-09-204-117B-5	Sequence 5, Appl1
2	93.3	1296	4	US-09-710-279-1473	Sequence 1473, Ap
3	93.3	1353	3	US-09-134-001C-1974	Sequence 1974, Ap
4	93.3	3017	4	US-09-710-279-4422	Sequence 4422, Ap
5	93.3	3233	4	US-09-710-279-3586	Sequence 3586, Ap
6	93.3	4185	4	US-09-710-279-3646	Sequence 3646, Ap
7	89.3	601	4	US-09-949-016-157837	Sequence 157837, Ap
8	89.3	1884	4	US-09-902-540-8567	Sequence 8567, Ap
9	89.3	11382	4	US-09-949-016-17537	Sequence 17537, Ap
10	89.3	79756	4	US-09-949-016-16143	Sequence 16143, A
11	86.7	601	4	US-09-949-016-132415	Sequence 132415, A
12	86.7	601	4	US-09-949-016-161664	Sequence 161664, A
13	86.7	601	4	US-09-949-016-15457	Sequence 15457, A
14	86.7	8264	4	US-09-949-016-15457	Sequence 15457, A
15	86.7	54531	4	US-09-949-016-15457	Sequence 15457, A
16	86.7	76962	4	US-09-949-016-15457	Sequence 15457, A
17	86.7	76962	4	US-09-949-016-15457	Sequence 15457, A
18	86.7	325791	4	US-09-768-185A-1	Sequence 1488, A
19	86.7	450395	4	US-09-949-016-15473	Sequence 15473, A
20	86.7	670689	4	US-09-949-016-12505	Sequence 12505, A
21	86.7	670689	4	US-09-949-016-12505	Sequence 12505, A
22	86.7	4403765	3	US-09-103-840A-2	Sequence 14207, A
23	86.7	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
24	82.7	25	4	US-09-386-196G-117504	Sequence 117504, A
25	82.7	25	4	US-09-386-196G-117515	Sequence 117515, A
26	82.7	25	4	US-09-386-196G-117517	Sequence 117517, A
27	82.7	258	4	US-09-107-532A-428	Sequence 428, App

ALIGNMENTS

28	12.4	82.7	265	4	US-09-513-999C-10978	Sequence 10978, A
29	12.4	82.7	362	4	US-09-513-999C-9915	Sequence 9915, Ap
30	12.4	82.7	434	4	US-09-270-767-4883	Sequence 4883, Ap
31	12.4	82.7	434	4	US-09-270-767-4883	Sequence 20165, A
32	12.4	82.7	525	4	US-09-252-931A-2828	Sequence 2828, Ap
33	12.4	82.7	540	2	US-08-448-561-3	Sequence 3, Appl1
34	12.4	82.7	774	4	US-09-270-767-2784	Sequence 2784, Ap
35	12.4	82.7	774	4	US-09-270-767-18066	Sequence 18066, A
36	12.4	82.7	1272	4	US-09-328-352-560	Sequence 560, App
37	12.4	82.7	1659	4	US-09-252-991A-9018	Sequence 9018, Ap
38	12.4	82.7	2031	2	US-08-448-561-2	Sequence 2, Appl1
39	12.4	82.7	2310	4	US-09-252-991A-3040	Sequence 3040, Ap
40	12.4	82.7	7374	4	US-09-252-991A-9100	Sequence 9100, Ap
41	12.4	82.7	7518	4	US-09-620-312D-1051	Sequence 1051, Ap
42	12.4	82.7	8931	3	US-09-051-019-1	Sequence 18066, A
43	12.4	82.7	15472	3	US-09-453-702B-71	Sequence 1, Appl1
44	12.4	82.7	49389	4	US-09-949-016-12547	Sequence 71, Appl1
45	12.4	82.7	49389	4	US-09-949-016-13630	Sequence 13630, A

RESULT 1
US-09-204-117B-5
Sequence 5, Application US/09204117B
Patent No. 6413768
GENERAL INFORMATION:
APPLICANT: Galen, James
TITLE OF INVENTION: PLASMID MAINTENANCE SYSTEM FOR ANTIGEN DELIVERY
FILE REFERENCE: 4135-101
CURRENT APPLICATION NUMBER: US/09/204,117B
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: m1ac feature
LOCATION: (1..7)
OTHER INFORMATION: mutated Shiga toxin segment
US-09-204-117B-5

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAACCTAGGGCGCA 15
DB 1 CTGAACCTAGGGCGCA 15

RESULT 2
US-09-710-279-1473
Sequence 1473, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1473
LENGTH: 1296
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 18:04:09, Search time 69.3063 Seconds

(without alignments)
10487.183 Million cell updates/sec

Title: US-10-750-976-37

Perfect score: 15

Sequence: 1 acagcagacgcctca 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: gb_ba:*
2: gb_mtg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	3959	14	AY547458	AY547458 Avian ort
2	100.0	21113	2	CR391962	CR391962 Dantio rer
3	93.3	714	9	HS4327219	HS4327219 Homo sapi
4	93.3	3312	3	AY433803	AY433803 Trypanoso
5	93.3	5069	5	AF038560	AF038560 Gallus ga
6	93.3	10221	1	AE014558	AE014558 Brucella
7	93.3	10495	1	AE009700	AE009700 Brucella
8	93.3	24523	1	AE008756	AE008756 Salmone1
9	93.3	36748	7	AY539836	AY539836 Burkholde
10	93.3	39949	3	AC009782	AC009782 Leishman1
11	93.3	106256	3	AC108135	AC108135 Leishman1
12	93.3	110000	2	AP006498	AP006498 7 of
13	93.3	133713	3	AC087838	AC087838 Leishman1
14	93.3	147226	9	AC103736	AC103736 Homo sapi
15	93.3	152770	9	AC013602	AC013602 Homo sapi
16	93.3	173839	9	AC026005	AC026005 Homo sapi
17	93.3	181097	2	AC118205	AC118205 Mus muscu
18	93.3	217285	2	AC126317	AC126317 Rattus no
19	93.3	233050	1	AL627271	AL627271 Salmone1

C 20	14	93.3	260760	2	AC127861	AC127861 Rattus no
C 21	14	93.3	295050	1	AL591982	AL591982 Ligetaria
C 22	14	93.3	300523	1	AE016838	AE016838 Salmone1
C 23	14	93.3	305325	1	AE016765	AE016765 Escherich
C 24	14	93.3	311600	1	AE016871	AE016871 Pseudomon
C 25	14	93.3	340750	1	BX294135	BX294135 Pirellula
C 26	14	93.3	349980	6	AK641671	AK641671 Sequence
C 27	13.4	89.3	155	8	HV19R	AK641671 Sequence
C 28	13.4	89.3	227	8	HVE1323LR	AK641671 Sequence
C 29	13.4	89.3	231	8	HVE1329TR	AK641671 Sequence
C 30	13.4	89.3	232	8	HVE1324MR	AK641671 Sequence
C 31	13.4	89.3	243	6	AR321328	AK641671 Sequence
C 32	13.4	89.3	318	6	AX048488	AX048488 Sequence
C 33	13.4	89.3	318	6	AX048489	AX048489 Sequence
C 34	13.4	89.3	356	8	HVE08492R	AX048489 Sequence
C 35	13.4	89.3	413	6	CO481384	AX048489 Sequence
C 36	13.4	89.3	640	14	AF322856	AF322856 Caprine a
C 37	13.4	89.3	798	6	AR388811	AR388811 Sequence
C 38	13.4	89.3	817	8	PSU58023	US8023 Pseudorogsn
C 39	13.4	89.3	858	11	CNS0603B	AL401085 T7 and of
C 40	13.4	89.3	1074	6	AR386605	AR386605 Sequence
C 41	13.4	89.3	1104	8	AB189674	AB189674 Philodend
C 42	13.4	89.3	1238	1	AB174823	AB174823 Cellulomo
C 43	13.4	89.3	1281	9	BC064028	BC064028 Homo sapi
C 44	13.4	89.3	1404	3	AF026516	AF026516 Funiculin
C 45	13.4	89.3	1539	6	AX568254	AX568254 Sequence

ALIGNMENTS

RESULT 1	AY547458	3959 bp	RNA	linear	VRL 04-AUG-2004
LOCUS	AY547458				
DEFINITION	Avian orthoreovirus inner capsid protein lambda-A gene, complete cds.				
ACCESSION	AY547458				
VERSION	AY547458.1	GI:47420812			
KEYWORDS	Avian orthoreovirus				
SOURCE	Avian orthoreovirus				
ORGANISM	Virus; dsRNA viruses; Reoviridae; Orthoreovirus.				
REFERENCE	1. (bases 1 to 3959)				
AUTHORS	Touris-Otero, F., Cortez-San Martin, M., Martinez-Coostas, J. and Benavente, J.				
TITLE	Avian Reovirus Morphogenesis Occurs Within Viral Factories and Begins with the Selective Recruitment of sigmans and lambda to MUNS Inclusions				
JOURNAL	J. Mol. Biol. 341 (2), 361-374 (2004)				
PUBMED	15276829				
REFERENCE	2. (bases 1 to 3959)				
AUTHORS	Cortez-San Martin, M., Touris-Otero, F., Martinez-Coostas, J. and Benavente, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-FEB-2004) Biogenetica, Universidad de Santiago de Compostela, Facultad de Farmacia Campus Sur s/n, Santiago de Compostela, La Coruna 15782, Spain				
FEATURES	Location/Qualifiers				
source	1. 3959				
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	/mol_type="genomic RNA"				
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	/segment="11"				
	/country="USA"				
	22. 3903				
	/codon_start=1				
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	/protein_id="AA27445.1"				
	/db_xref="GI:47420813"				
	/translation="MSSRRVARRRHKDADTESKDTQTKSKRSSIDAKESDTSDADKX VTAAPPNPAASTPSSTDCASGTSYAKQTHHDASVKSAPETVSSGKQDHWGAVK SODAKATVAVDNNKDRDVPFGAGSGDKNALITKTSVNDNGVKKVPAKADATISSAKA				

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:32:44 ; Search time 20.7192 Seconds

(without alignments)
9714.213 Million cell updates/sec

Title: US-10-750-976-36

Perfect score: 34
Sequence: 1 agatcmtaancatccacagagagatctgcatg 34

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn19908.*
3: geneseqn20008.*
4: geneseqn20018.*
5: geneseqn20028.*
6: geneseqn20038.*
7: geneseqn20048.*
8: geneseqn20058.*
9: geneseqn20068.*
10: geneseqn20078.*
11: geneseqn20088.*
12: geneseqn20098.*
13: geneseqn20108.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	76.5	33	3	AAA07572 Modified
2	26	76.5	4196	3	AAA030825 Expressio
3	23	67.6	32	3	AAA07567 Modified
4	22.8	67.1	59	3	AAA030809 PCR prime
5	22.2	65.3	349	5	ABV09570 Human pro
6	22.2	65.3	400	5	ABV0746 Human pro
7	22.2	65.3	400	5	ABV0746 Human pro
8	21.2	62.4	33	2	AAQ24139 Leader p
9	21.2	62.4	3712	2	AAQ97490 Plasmid p
10	21.2	62.4	3754	2	AAQ97490 Plasmid p
11	21.2	62.4	3754	2	AAQ97490 Plasmid p
12	21.2	62.4	3754	2	AAQ97490 Plasmid p
13	21.2	62.4	3754	2	AAQ97490 Plasmid p
14	21.2	62.4	3754	2	AAQ97490 Plasmid p
15	21.2	62.4	3754	2	AAQ97490 Plasmid p
16	20.6	60.6	700	4	AAH92629 Human int
17	19.8	58.2	77287	6	ABV2623 Murine tu
18	19.8	58.2	82938	6	ABV2623 Murine tu
19	19.8	58.2	110000	13	ABV2623 Murine tu
20	19.8	58.2	167739	9	AAH58258 Murine tu

21	19.6	57.6	414	10	ADH59176 Rat gene
22	19.6	57.6	650	3	AAH51918 Arabidops
23	19.6	57.6	782	3	AAH51918 Arabidops
24	19.6	57.6	879	6	ABH21388 Arabidops
25	19.6	57.6	1051	6	ABH21388 Arabidops
26	19.6	57.6	1140	3	AAH51918 Arabidops
27	19.6	57.6	1189	3	AAH51918 Arabidops
28	19.4	57.1	1907	4	AAH51918 Arabidops
29	19.4	57.1	2152	4	AAH51918 Arabidops
30	19.4	57.1	2152	4	AAH51918 Arabidops
31	19.4	57.1	2152	4	AAH51918 Arabidops
32	19.4	57.1	2152	4	AAH51918 Arabidops
33	19.4	57.1	2152	4	AAH51918 Arabidops
34	19.4	57.1	2152	4	AAH51918 Arabidops
35	18.8	55.3	496	13	ADH59176 Rat gene
36	18.8	55.3	1497	10	ADH59176 Rat gene
37	18.8	55.3	1764	10	ADH59176 Rat gene
38	18.8	55.3	1764	10	ADH59176 Rat gene
39	18.8	55.3	28903	11	ACN44636 Mouse gen
40	18.8	55.3	32249	4	AAH51918 Arabidops
41	18.8	55.3	32249	4	AAH51918 Arabidops
42	18.8	55.3	170834	10	ADH59176 Rat gene
43	18.8	55.3	192427	10	ADH59176 Rat gene
44	18.8	55.3	214019	10	ADH59176 Rat gene
45	18.8	55.3	319608	3	AAH51601 Human chr

ALIGNMENTS

RESULT 1	AAA07572	standard; DNA; 33 BP.
ID	AAA07572	standard; DNA; 33 BP.
AC	AAA07572	standard; DNA; 33 BP.
XX	29-AUG-2000	(first entry)
DT	XX	
DE	Modified ompC promoter.	
XX	Expression cassette; plasmid maintenance system; Neisseria meningitidis;	
KW	post-segregational killing function; ompC promoter; immune response;	
KW	vaccine; Salmonella typhi; hepatitis; Haemophilus influenzae type b;	
KW	acellular pertussis; varicella; rotavirus; Streptococcus pneumoniae;	
KW	cancer vaccine; autoimmune disorder; immunological disease; allergy;	
KW	myasthenia gravis; lupus erythematosus; rheumatoid arthritis; therapy;	
KW	multiple sclerosis; asthma; ss.	
XX	Unidentified.	
OS	Unidentified.	
XX	Unidentified.	
PN	WO200032047-A1.	
PD	08-JUN-2000.	
XX	02-DEC-1999;	99WO-US028499.
PF	02-DEC-1999;	98US-00204117.
XX	12-OCT-1999;	99US-0158738P.
PR	(UYMA-) UNIV MARYLAND BALTIMORE.	
XX	Galen UE;	
PI	WPI, 2000-412091/35.	
XX	Expression cassette used as live vector vaccine comprises nucleotide	
PT	sequence encoding origin of replication and plasmid maintenance system	
PT	which includes a post-segregational killing and a partitioning function.	
PS	Claim 145; Page 102; 127P; English.	
XX	This sequence represents a modified ompC promoter, and can be used in the	
CC	expression cassette of the invention. The cassette is an independently	

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 18:04:09 ; Search time 19387.3 Seconds
(without alignments)
10487.183 Million cell updates/sec

Title: US-10-750-976-1

Perfect score: 4196
Sequence: 1 gaattctgtggtcagacaga.....cctcccgagttgtcctcga 4196

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 2: gb_hcg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pat:*
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- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_scs:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4196	100.0	4196	6 AR483257	AR483257 Sequence
2	1707.8	40.7	2646	12 ASPMIN3	Z50149 Artificial
3	1704.6	40.6	2538	12 ASPMIN1	Z50148 Artificial
4	1672.8	39.9	6271	6 AX718406	AX718406 Sequence
5	1613	38.4	6349	12 AF047519	AF047519 Cloning v
6	1571.8	37.5	8121	12 SC0302086	AJ302086 Synthetic
7	1540.2	36.7	4939	6 BD263381	BD263381 Composite
8	1534.6	36.6	4977	12 U07168	U07168 Cloning vec
9	1533	36.5	5610	12 AF140576	AF140576 Integrati
10	1533	36.5	6370	12 AF140578	AF140578 Integrati
11	1533	36.5	8875	12 AF140579	AF140579 Integrati
12	1533	36.5	12538	12 AF251497	AF251497 Cloning v
13	1489.6	35.5	5226	12 AF061924	AF061924 Plasmid
14	1489.6	35.5	6060	12 AF061927	AF061927 Plasmid
15	1489.6	35.5	6060	12 AF061928	AF061928 Plasmid
16	1428.2	34.0	6755	12 AF140577	AF140577 Integrati
17	1420.8	33.9	8908	6 AX718423	AX718423 Sequence
18	1193	28.4	8908	6 AX718423	AX718423 Sequence
19	1192.8	28.4	3274	12 SYNBR327V	L08856 pBR327 clon

20	1192.8	28.4	3301	6 AR287566	AR287566 Sequence
21	1192.8	28.4	3423	6 AR287564	AR287564 Sequence
22	1192.8	28.4	3474	6 A28084	A28084 pMTNF-MPH p
23	1192.8	28.4	3474	6 A28085	A28085 pMTNF-MPH p
24	1192.8	28.4	3474	6 A75741	A75741 Sequence 10
25	1192.8	28.4	3474	6 AR085100	AR085100 Sequence
26	1192.8	28.4	3474	6 AR209770	AR209770 Sequence
27	1192.8	28.4	3474	6 AR287565	AR287565 Sequence
28	1192.8	28.4	3658	12 SYNPR153V	L08853 pBR327 clon
29	1192.8	28.4	3668	12 SYNPR327P	L08857 pBR327par c
30	1192.8	28.4	3773	12 SYNPR751V	L09154 pMT551 exp
31	1192.8	28.4	3773	12 SYNPR751V	L09155 pMT571 exp
32	1192.8	28.4	3801	6 AR493833	AR493833 Sequence
33	1192.8	28.4	3809	12 SYNPR751V	L09153 pMT511 exp
34	1192.8	28.4	4009	6 A39734	A39734 Sequence 2
35	1192.8	28.4	4009	6 AR069625	AR069625 Sequence
36	1192.8	28.4	4245	6 AR069365	AR069365 Sequence
37	1192.8	28.4	4245	12 PACYC184	X06403 Cloning vec
38	1192.8	28.4	4342	12 SCUS4830	U54830 Cloning vec
39	1192.8	28.4	4361	12 SYNBR322	A055345 Cloning vec
40	1192.8	28.4	4442	12 AF055345	AF055345 Cloning vec
41	1192.8	28.4	4633	6 A20355	A20355 plasmid pIG
42	1192.8	28.4	4633	6 A20356	A20356 plasmid pIG
43	1192.8	28.4	4753	12 AF129432	AF129432 Cloning v
44	1192.8	28.4	4840	6 AX084356	AX084356 Sequence
45	1192.8	28.4	4907	12 SYNBR328V	L08858 pBR328 clon

ALIGNMENTS

RESULT 1	AR483257	Sequence 1 from patent US 6703233.	DNA	Linear	PAT 14-MAY-2004
LOCUS	AR483257	Sequence 1 from patent US 6703233.	DNA	Linear	PAT 14-MAY-2004
DEFINITION	AR483257	Sequence 1 from patent US 6703233.	DNA	Linear	PAT 14-MAY-2004
ACCESSION	AR483257	Sequence 1 from patent US 6703233.	DNA	Linear	PAT 14-MAY-2004
VERSION	AR483257.1	GI:47245788	DNA	Linear	PAT 14-MAY-2004
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 4196)				
AUTHORS	Galen, J.B.				
TITLE	Plasmid maintenance system for antigen delivery				
JOURNAL	Patent: US 6703233-A 1 09-MAR-2004;				
FEATURES	Location/Qualifiers				
source	1..4196				
ORIGIN	/mol_type="genomic DNA"				
Query Match	100.0%; Score 4196; DB 6; Length 4196;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches	4196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GAATTCGTGCTGACACAGATATGAAAAGTGTAAAGAGGTTAAAAAAGCGAAT 60				
DB	1 GAATTCGTGCTGACACAGATATGAAAAGTGTAAAGAGGTTAAAAAAGCGAAT 60				
QY	61 GCGAGGATCGGTTGAAATAGGGGTAAACAGACATTCGAATGAATGACGGTAAAT 120				
DB	61 GCGAGGATCGGTTGAAATAGGGGTAAACAGACATTCGAATGAATGACGGTAAAT 120				
QY	121 TAAAGTTAATGATGATAGCGGAGTATTTCTAGTTCGAGTGAAGTTTGTTCGAT 180				
DB	121 TAAAGTTAATGATGATAGCGGAGTATTTCTAGTTCGAGTGAAGTTTGTTCGAT 180				
QY	181 TCGTGTCTGCAATCTTAAGAAATGATTGATTTTAACTTGAATTTATTTGCTT 240				
DB	181 TCGTGTCTGCAATCTTAAGAAATGATTGATTTTAACTTGAATTTATTTGCTT 240				
QY	241 GAGTTAGGTCCTTATTTGGCCATTCGCAATATATCTTAAAGTCCCTGATTTAC 300				
DB	241 GAGTTAGGTCCTTATTTGGCCATTCGCAATATATCTTAAAGTCCCTGATTTAC 300				

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 11:14:05 / Search time 83.643 Seconds
(without alignments)
8669.645 Million cell updates/sec

Title: US-10-750-965-39
Perfect score: 15
Sequence: 1 gaattcgagaccagc 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_da:
2: gb_hlg:
3: gb_in:
4: gb_mn:
5: gb_ov:
6: gb_pac:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	1924	AK129669	AK129669 Homo sapi
2	15	100.0	3137	NCR243517	AJ243517 Neurospor
3	15	100.0	3566	EX119906	EX119906 Human DNA
4	15	100.0	17966	AC138145	AC138145 Homo sapi
5	15	100.0	190107	AC100832	AC100832 Homo sapi
6	15	100.0	349841	BX572606	BX572606 Rhodosphe
7	15	93.3	385	CO472848	CO472848 Sequence
8	14	93.3	396	CO478754	CO478754 Sequence
9	14	93.3	417	CO465886	CO465886 Sequence
10	14	93.3	428	CO482017	CO482017 Sequence
11	14	93.3	430	CO503156	CO503156 Sequence
12	14	93.3	438	CO499951	CO499951 Sequence
13	14	93.3	438	CO508919	CO508919 Sequence
14	14	93.3	438	CO512005	CO512005 Sequence
15	14	93.3	459	CO692166	CO692166 Sequence
16	14	93.3	559	BD152296	BD152296 Primer fo
17	14	93.3	559	AX872234	AX872234 Sequence
18	14	93.3	594	CO489052	CO489052 Sequence
19	14	93.3	594	CO491123	CO491123 Sequence

C 20	14	93.3	594	6	CO494900	CO494900 Sequence
C 21	14	93.3	594	6	CO496987	CO496987 Sequence
C 22	14	93.3	966	13	AY487538	AY487538 Unculture
C 23	14	93.3	1200	6	AR376947	AR376947 Sequence
C 24	14	93.3	1521	1	AF411070	AF411070 Sphingomo
C 25	14	93.3	1681	9	AK000455	AK000455 Homo sapi
C 26	14	93.3	2133	6	BD159467	BD159467 Primer fo
C 27	14	93.3	2133	6	AX882028	AX882028 Sequence
C 28	14	93.3	2133	9	AK027380	AK027380 Homo sapi
C 29	14	93.3	2075	1	AF127079	AF127079 Salmonell
C 30	14	93.3	7119	3	AF329639	AF329639 Drosophil
C 31	14	93.3	21470	1	AE008733	AE008733 Salmone11
C 32	14	93.3	43596	9	AC091886	AC091886 Homo sapi
C 33	14	93.3	56883	2	AL365182	AL365182 Human DNA
C 34	14	93.3	60752	2	AC105060	AC105060 Mus muscu
C 35	14	93.3	119184	1	D90909	D90909 Synchocyst
C 36	14	93.3	119638	9	AC024575	AC024575 Homo sapi
C 37	14	93.3	132492	9	AC007616	AC007616 Homo sapi
C 38	14	93.3	142645	9	AC008481	AC008481 Homo sapi
C 39	14	93.3	144000	9	AC007621	AC007621 Homo sapi
C 40	14	93.3	144771	2	AC018610	AC018610 Homo sapi
C 41	14	93.3	152081	9	AC007381	AC007381 Homo sapi
C 42	14	93.3	153049	9	BS000182	BS000182 Pan trogl
C 43	14	93.3	163384	9	AC009180	AC009180 Homo sapi
C 44	14	93.3	164008	2	AC024064	AC024064 Homo sapi
C 45	14	93.3	169250	9	AP002812	AP002812 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AK129669
DEFINITION Homo sapiens cDNA FL26158 f1s, clone ADG01579.
ACCESSION AK129669
VERSION AK129669.1 GI:34526262
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isegai, T., Sugiyama, S., NEDO human cDNA sequencing project
2 (bases 1 to 1924)
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-da, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: f1cdna@life.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology (RAB): cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
Location/Qualifiers
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/mol_type="cDNA"
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/clone="ADG01579"
/issue_type="adrenal gland"
/clone_lib="ADG"

FEATURES

source

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: April 26, 2005, 11:14:05 ; Search time 6674.71 Seconds
(without alignments)
8689.645 Million cell updates/sec

Title: US-10-750-965-2
1197

Perfect score: 1 ctacataatagagctagcc.....gagcgaacggggagagcag 1197
Sequence:

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ha:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pi:*
10: gb_ro:*
11: gb_ey:*
12: gb_ey:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197	100.0	1197	6 AR483258	AR483258 Sequence
2	817.4	68.3	4196	6 AR483257	AR483257 Sequence
3	718.2	60.0	6271	6 AX718406	AX718406 Sequence
4	718.2	60.0	8908	6 AX718423	AX718423 Sequence
5	627.4	52.4	1026	1 ECP15A	U00309 E. coli pla
6	627.4	52.4	2314	1 AP432497	AP432497 Escherich
7	627.4	52.4	2553	12 CVE289102	AJ289102 Cloning v
8	627.4	52.4	2558	12 CVE27764	AJ277764 Cloning v
9	627.4	52.4	3210	12 AF361440	AF361440 Cloning v
10	627.4	52.4	3465	6 AX000478	AX000478 Sequence
11	627.4	52.4	3465	6 BD073379	BD073379 Process f
12	627.4	52.4	3481	6 AX000480	AX000480 Sequence
13	627.4	52.4	3481	6 BD073380	BD073380 Process f
14	627.4	52.4	3666	12 U66309	U66309 Expression
15	627.4	52.4	3720	6 BD136661	BD136661 Sequence
16	627.4	52.4	3720	6 AX018968	AX018968 Sequence
17	627.4	52.4	3794	6 BD136662	BD136662 Process f
18	627.4	52.4	3794	6 AX000474	AX000474 Sequence
19	627.4	52.4	3794	6 AX018970	AX018970 Sequence

20	627.4	52.4	3794	6 BD073377	BD073377 Process f
21	627.4	52.4	3801	6 AR493833	AR493833 Sequence
22	627.4	52.4	3810	6 AX000476	AX000476 Sequence
23	627.4	52.4	3810	6 BD073378	BD073378 Process f
24	627.4	52.4	4245	6 AR069365	AR069365 Sequence
25	627.4	52.4	4245	12 PACYC184	X06403 Cloning vec
26	627.4	52.4	4411	6 AR069366	AR069366 Sequence
27	627.4	52.4	4753	12 AP129432	AP129432 Cloning v
28	627.4	52.4	4975	6 BD136663	BD136663 Process f
29	627.4	52.4	4975	6 AX018972	AX018972 Sequence
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31	627.4	52.4	5201	6 AR493834	AX799953 Sequence
32	627.4	52.4	5201	6 AR493835	AR493834 Sequence
33	627.4	52.4	5835	13 CVU47103	AR493835 Sequence
34	627.4	52.4	6101	12 SIN417488	U47103 Cloning vec
35	627.4	52.4	6123	12 SIN417489	AJ117488 Shuttle 1
36	627.4	52.4	6363	6 AR069367	AJ117449 Shuttle 1
37	627.4	52.4	6758	12 AF121784	AR069367 Sequence
38	627.4	52.4	8774	12 AY042185	AF121784 Expression
39	627.4	52.4	8774	12 IVU69267	AY042185 Cloning v
40	627.4	52.4	9065	12 AF405698	U69267 Integration
41	627.4	52.4	12168	12 AF405696	AF405698 Reporter
42	627.4	52.4	12248	12 AF405697	AF405696 Reporter
43	627.4	52.4	14928	12 AY230218	AY230218 Expression
44	627.4	52.4	18658	12 XXU73849	U73849 Synthetic c
45	626.2	52.3	4523	12 EVE243540	AJ243540 Expression

ALIGNMENTS

RESULT 1	AR483258	Sequence 2 from patent US 6703233.	1197 bp	DNA	linear	PAT 14-MAY-2004
LOCUS	AR483258					
DEFINITION	Sequence 2 from patent US 6703233.					
ACCESSION	AR483258					
VERSION	AR483258.1	GI:47245789				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 1197)					
TITLE	Galen, J.E.					
JOURNAL	Plasmid maintenance system for antigen delivery					
FEATURES	Patent: US 6703233-A2 09-MAR-2004;					
source	Location/Qualifiers					
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	/mol_type="genomic DNA"					
Query Match	100.0%;	Score 1197;	DB 6;	Length 1197;		
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DB	1	CTACAATATATGAGCTAGCCGCTAATGAGCGGCTTTTCTTCTGCGCTAGAGATA	60			
QY	61	CTTACAGGAGATGAGAGCGCGGCAAGCGTTTTCATDAGGCTCGGCCCTG	120			
DB	61	CTTACAGGAGATGAGAGCGCGGCAAGCGTTTTCATDAGGCTCGGCCCTG	120			
QY	121	ACAAGATCAAGAAATCTGCTCAATCATGCTGCGGAAACCGACAGACTATAA	180			
DB	121	ACAAGATCAAGAAATCTGCTCAATCATGCTGCGGAAACCGACAGACTATAA	180			
QY	181	GATACAGGCGTTTCCCGTGGCGGCTCTCTGCTCTCTCTCTCTCTCTCTCTCT	240			
DB	181	GATACAGGCGTTTCCCGTGGCGGCTCTCTGCTCTCTCTCTCTCTCTCTCTCT	240			
QY	241	TTACCGGTCTCATTCGCTGTATAGCGCGGTTTGTCTCATTCACGCTGACCTCAGT	300			
DB	241	TTACCGGTCTCATTCGCTGTATAGCGCGGTTTGTCTCATTCACGCTGACCTCAGT	300			